

# SEQUENCE LISTING

<110> Johansen, et al.

<120> Method

<130> 674509-2025

<140> 09/722,938

<141> 2000-11-27

<150> PCT/IB 00/01886

<151> 2000-11-24

<150> GB 9927801.2

<151> 1999-11-24

<160> 28

<170> PatentIn version 3.0

<210> 1

<211> 10

<212> PRT

<213> Artificial

<220>

<223> Description of Artificial Sequence: N-terminal sequence

<400> 1

Ala	Thr	Leu	Pro	Gln	Lys	Asp	Pro	Gly	Tyr
1				5					10

<210> 2

<211> 61

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 2

actccatggc	tactttgcc	caaaaggacc	caggttacat	tggtattgac	gtcaacgctg	60
g						61

<210> 3

<211> 107

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 3

cgaaatcgat gttggtacca atccatcttc tgttgaaacc ttgcttcacg gatggcaatc 60  
 ttgggtcagg cttgtctgga gtaccagcgt tgacgtcaat aacaatg 107

<210> 4  
 <211> 106  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 4  
 gattggtacc aacatcgatt tcgtttacgt cgtttacact ccacaagggtg cttgtactgc 60  
 tttggacaga gctatggaaa agtgttctcc aggtaccgtc agaatc 106

<210> 5  
 <211> 106  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 5  
 ttcaacccaaa ccagtaacgt tgataatagc cttgacacat tcgtcgaaaa cgaagtcttc 60  
 gtaacagtga ccaccagaaa cgattctgac ggtacctgga gaacac 106

<210> 6  
 <211> 120  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 6  
 atcaacgtta ctggtttggt tgaatctggt tacgacgacg atagaggta cttcgtctct 60  
 tccggtgaca ccaactgggg ttccttcaag accttggtca gagaccacgg tagagttttg 120

<210> 7  
 <211> 109  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 7  
 caaacctgac aatctggcca aaataaccgtc acctccaccg acaatgtgac caccctaaacc 60

gacggagtaa caggaaccac ctggcaaaac tctaccgtgg tctctgaac 109

<210> 8

<211> 109

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 8

tttggccaga ttgcacggtt tgccagtoga ttggttatcc ggtgttgaag ttgtcgtaa 60

gccagtcttg accgaagact ctgttcttaa gtacgttcac aaggattcc 109

<210> 9

<211> 116

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 9

ggcaaactct tgaagtagta tttggtgata ataccgaagt tacctccacc tccaccagtg 60

tgagcccaaa acaactcacc gtcgttacct tcggaatcct tgtgaacgta ctttaag 116

<210> 10

<211> 118

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 10

caaatactac ttcaaggatt tgccaatgtc tccaagaggt gtcacgctt ctaacttaca 60

cttctcttgg gacggtttca ctagagatgc cttgcaagat ttgttgacta agtacttc 118

<210> 11

<211> 118

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 11

ggaggtatac aagtacataa caaactcttc agctgcttgg tggaagattt ggaacttacc 60

aacagtattc ttccaatcac atctagccaa cttgaagtac ttagtcaaca aatcttgc 118

<210> 12

<211> 96

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 12

atcttccatc aggcagctga agagtttggt atgtacttgt atacatccta ctctaacgac 60

gccgagagag aagttgcccc agacagacac tatcat 96

<210> 13

<211> 102

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 13

gaaaggagcc caaccagcat gaccaccaag agctttggta ggctcgcatg ttttgtagat 60

ctgttcaatg tcagcctcca aatgatagtg tctgtcttgg gc 102

<210> 14

<211> 90

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 14

gctgggtggg ctcccttccc tgtagacct agacctagac acacatccaa gacttcttat 60

atgcatgacg agactatgga ctaccctttc 90

<210> 15

<211> 120

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 15

aatctggaag tctggaaagt ccttgatcat gtaagcagac ttgtacttac ctctctgatt 60

aggaccggaa ccgttgatag tctcagtcaa agcgtagaaa gggtagtcca tagtctcgtc 120

<210> 16  
<211> 108  
<212> DNA  
<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 16  
gactttccag acttccagat tgatgttatc tggaaatacc ttactgaggt tcttgacggt 60  
ttgactagtg ccgaaatgaa ggatgctctt cttcaggttg atatgttc 108

<210> 17  
<211> 126  
<212> DNA  
<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 17  
cttgtcttct tcttgccagt atgtctggta ctgcagtttg atgatgtact ctctctgagc 60  
aactgcagta gcatcccaaa caaccttggt aatctcacca ccgaacatat caacctgaag 120  
aagagc 126

<210> 18  
<211> 108  
<212> DNA  
<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 18  
acatactggc aggaagaaga caaggatgca gttaacttga agtggattag agacttttac 60  
gaggagatgt atgagcctta tgggtggtgt ccagacccta acactcag 108

<210> 19  
<211> 111  
<212> DNA  
<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 19  
ggcaccatac ttaccgttct tccagttggt caagtcaaca tcagggtagt tgaagtagca 60

tccctcaaaa acacctttac cactctcaac ctgagtgtta gggctctggaa c 111

<210> 20  
<211> 117  
<212> DNA  
<213> Artificial

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 20  
aagaacggta agtatgggtgc cttggaactt tacttttttg gtaacctgaa cagattgatc 60  
aaggccaaat ggttgtggga tcctaacgag atcttcacaa acaaacagtc tatecct 117

<210> 21  
<211> 78  
<212> DNA  
<213> Artificial

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 21  
gaattccgcg gccgcctact atttagtctg cttaggctcc ttaagagggt tagtagggat 60  
agactgtttg tttgtgaa 78

<210> 22  
<211> 1644  
<212> DNA  
<213> Artificial

<220>  
<223> nucleotide sequence of synthetic Hox gene

<220>  
<221> CDS  
<222> (1)..(1644)  
<223> coding sequence of synthetic HOX gene

<400> 22  
atg gct act ttg cca caa aag gac cca ggt tac att gtt att gac gtc 48  
Met Ala Thr Leu Pro Gln Lys Asp Pro Gly Tyr Ile Val Ile Asp Val  
1 5 10 15

aac gct ggt act cca gac aag cct gac cca aga ttg cca tcc atg aag 96  
Asn Ala Gly Thr Pro Asp Lys Pro Asp Pro Arg Leu Pro Ser Met Lys  
20 25 30

caa ggt ttc aac aga aga tgg att ggt acc aac atc gat ttc gtt tac 144  
Gln Gly Phe Asn Arg Arg Trp Ile Gly Thr Asn Ile Asp Phe Val Tyr  
35 40 45

gtc gtt tac act cca caa ggt gct tgt act gct ttg gac aga gct atg	192
Val Val Tyr Thr Pro Gln Gly Ala Cys Thr Ala Leu Asp Arg Ala Met	
50 55 60	
gaa aag tgt tct cca ggt acc gtc aga atc gtt tct ggt ggt cac tgt	240
Glu Lys Cys Ser Pro Gly Thr Val Arg Ile Val Ser Gly Gly His Cys	
65 70 75 80	
tac gaa gac ttc gtt ttc gac gaa tgt gtc aag gct att atc aac gtt	288
Tyr Glu Asp Phe Val Phe Asp Glu Cys Val Lys Ala Ile Ile Asn Val	
85 90 95	
act ggt ttg gtt gaa tct ggt tac gac gac gat aga ggt tac ttc gtc	336
Thr Gly Leu Val Glu Ser Gly Tyr Asp Asp Asp Arg Gly Tyr Phe Val	
100 105 110	
tct tcc ggt gac acc aac tgg ggt tcc ttc aag acc ttg ttc aga gac	384
Ser Ser Gly Asp Thr Asn Trp Gly Ser Phe Lys Thr Leu Phe Arg Asp	
115 120 125	
cac ggt aga gtt ttg cca ggt ggt tcc tgt tac tcc gtc ggt ttg ggt	432
His Gly Arg Val Leu Pro Gly Gly Ser Cys Tyr Ser Val Gly Leu Gly	
130 135 140	
ggt cac att gtc ggt gga ggt gac ggt att ttg gcc aga ttg cac ggt	480
Gly His Ile Val Gly Gly Gly Asp Gly Ile Leu Ala Arg Leu His Gly	
145 150 155 160	
ttg cca gtc gat tgg tta tcc ggt gtt gaa gtt gtc gtt aag cca gtc	528
Leu Pro Val Asp Trp Leu Ser Gly Val Glu Val Val Val Lys Pro Val	
165 170 175	
ttg acc gaa gac tct gtt ctt aag tac gtt cac aag gat tcc gaa ggt	576
Leu Thr Glu Asp Ser Val Leu Lys Tyr Val His Lys Asp Ser Glu Gly	
180 185 190	
aac gac ggt gag ttg ttt tgg gct cac act ggt gga ggt gga ggt aac	624
Asn Asp Gly Glu Leu Phe Trp Ala His Thr Gly Gly Gly Gly Gly Asn	
195 200 205	
ttc ggt att atc acc aaa tac tac ttc aag gat ttg cca atg tct cca	672
Phe Gly Ile Ile Thr Lys Tyr Tyr Phe Lys Asp Leu Pro Met Ser Pro	
210 215 220	
aga ggt gtc atc gct tct aac tta cac ttc tct tgg gac ggt ttc act	720
Arg Gly Val Ile Ala Ser Asn Leu His Phe Ser Trp Asp Gly Phe Thr	
225 230 235 240	
aga gat gcc ttg caa gat ttg ttg act aag tac ttc aag ttg gct aga	768
Arg Asp Ala Leu Gln Asp Leu Leu Thr Lys Tyr Phe Lys Leu Ala Arg	
245 250 255	
tgt gat tgg aag aat act gtt ggt aag ttc caa atc ttc cac caa gca	816
Cys Asp Trp Lys Asn Thr Val Gly Lys Phe Gln Ile Phe His Gln Ala	
260 265 270	

gct gaa gag ttt gtt atg tac ttg tat aca tcc tac tct aac gac gcc Ala Glu Glu Phe Val Met Tyr Leu Tyr Thr Ser Tyr Ser Asn Asp Ala 275 280 285	864
gag aga gaa gtt gcc caa gac aga cac tat cat ttg gag gct gac att Glu Arg Glu Val Ala Gln Asp Arg His Tyr His Leu Glu Ala Asp Ile 290 295 300	912
gaa cag atc tac aaa aca tgc gag cct acc aaa gct ctt ggt ggt cat Glu Gln Ile Tyr Lys Thr Cys Glu Pro Thr Lys Ala Leu Gly Gly His 305 310 315 320	960
gct ggt tgg gct cct ttc cct gtt aga cct aga aag aga cac aca tcc Ala Gly Trp Ala Pro Phe Pro Val Arg Pro Arg Lys Arg His Thr Ser 325 330 335	1008
aag act tct tat atg cat gac gag act atg gac tac cct ttc tac gct Lys Thr Ser Tyr Met His Asp Glu Thr Met Asp Tyr Pro Phe Tyr Ala 340 345 350	1056
ttg act gag act atc aac ggt tcc ggt cct aat cag aga ggt aag tac Leu Thr Glu Thr Ile Asn Gly Ser Gly Pro Asn Gln Arg Gly Lys Tyr 355 360 365	1104
aag tct gct tac atg atc aag gac ttt cca gac ttc cag att gat gtt Lys Ser Ala Tyr Met Ile Lys Asp Phe Pro Asp Phe Gln Ile Asp Val 370 375 380	1152
atc tgg aaa tac ctt act gag gtt cct gac ggt ttg act agt gcc gaa Ile Trp Lys Tyr Leu Thr Glu Val Pro Asp Gly Leu Thr Ser Ala Glu 385 390 395 400	1200
atg aag gat gct ctt ctt cag gtt gat atg ttc ggt ggt gag att cac Met Lys Asp Ala Leu Leu Gln Val Asp Met Phe Gly Gly Glu Ile His 405 410 415	1248
aag gtt gtt tgg gat gct act gca gtt gct cag aga gag tac atc atc Lys Val Val Trp Asp Ala Thr Ala Val Ala Gln Arg Glu Tyr Ile Ile 420 425 430	1296
aaa ctg cag tac cag aca tac tgg cag gaa gaa gac aag gat gca gtt Lys Leu Gln Tyr Gln Thr Tyr Trp Gln Glu Glu Asp Lys Asp Ala Val 435 440 445	1344
aac ttg aag tgg att aga gac ttt tac gag gag atg tat gag cct tat Asn Leu Lys Trp Ile Arg Asp Phe Tyr Glu Glu Met Tyr Glu Pro Tyr 450 455 460	1392
ggt ggt gtt cca gac cct aac act cag gtt gag agt ggt aaa ggt gtt Gly Gly Val Pro Asp Pro Asn Thr Gln Val Glu Ser Gly Lys Gly Val 465 470 475 480	1440
ttt gag gga tgc tac ttc aac tac cct gat gtt gac ttg aac aac tgg Phe Glu Gly Cys Tyr Phe Asn Tyr Pro Asp Val Asp Leu Asn Asn Trp 485 490 495	1488
aag aac ggt aag tat ggt gcc ttg gaa ctt tac ttt ttg ggt aac ctg	1536



Lys Asn Gly Lys Tyr Gly Ala Leu Glu Leu Tyr Phe Leu Gly Asn Leu  
500 505 510

aac aga ttg atc aag gcc aaa tgg ttg tgg gat cct aac gag atc ttc 1584  
Asn Arg Leu Ile Lys Ala Lys Trp Leu Trp Asp Pro Asn Glu Ile Phe  
515 520 525

aca aac aaa cag tct atc cct act aaa cct ctt aag gag cct aag cag 1632  
Thr Asn Lys Gln Ser Ile Pro Thr Lys Pro Leu Lys Glu Pro Lys Gln  
530 535 540

act aaa tag tag 1644  
Thr Lys  
545

<210> 23  
<211> 546  
<212> PRT  
<213> Artificial

<400> 23

Met Ala Thr Leu Pro Gln Lys Asp Pro Gly Tyr Ile Val Ile Asp Val  
1 5 10 15

Asn Ala Gly Thr Pro Asp Lys Pro Asp Pro Arg Leu Pro Ser Met Lys  
20 25 30

Gln Gly Phe Asn Arg Arg Trp Ile Gly Thr Asn Ile Asp Phe Val Tyr  
35 40 45

Val Val Tyr Thr Pro Gln Gly Ala Cys Thr Ala Leu Asp Arg Ala Met  
50 55 60

Glu Lys Cys Ser Pro Gly Thr Val Arg Ile Val Ser Gly Gly His Cys  
65 70 75 80

Tyr Glu Asp Phe Val Phe Asp Glu Cys Val Lys Ala Ile Ile Asn Val  
85 90 95

Thr Gly Leu Val Glu Ser Gly Tyr Asp Asp Asp Arg Gly Tyr Phe Val  
100 105 110

Ser Ser Gly Asp Thr Asn Trp Gly Ser Phe Lys Thr Leu Phe Arg Asp  
115 120 125

His Gly Arg Val Leu Pro Gly Gly Ser Cys Tyr Ser Val Gly Leu Gly  
130 135 140

Gly His Ile Val Gly Gly Gly Asp Gly Ile Leu Ala Arg Leu His Gly  
 145 150 155 160

Leu Pro Val Asp Trp Leu Ser Gly Val Glu Val Val Val Lys Pro Val  
 165 170 175

Leu Thr Glu Asp Ser Val Leu Lys Tyr Val His Lys Asp Ser Glu Gly  
 180 185 190

Asn Asp Gly Glu Leu Phe Trp Ala His Thr Gly Gly Gly Gly Gly Asn  
 195 200 205

Phe Gly Ile Ile Thr Lys Tyr Tyr Phe Lys Asp Leu Pro Met Ser Pro  
 210 215 220

Arg Gly Val Ile Ala Ser Asn Leu His Phe Ser Trp Asp Gly Phe Thr  
 225 230 235 240

Arg Asp Ala Leu Gln Asp Leu Leu Thr Lys Tyr Phe Lys Leu Ala Arg  
 245 250 255

Cys Asp Trp Lys Asn Thr Val Gly Lys Phe Gln Ile Phe His Gln Ala  
 260 265 270

Ala Glu Glu Phe Val Met Tyr Leu Tyr Thr Ser Tyr Ser Asn Asp Ala  
 275 280 285

Glu Arg Glu Val Ala Gln Asp Arg His Tyr His Leu Glu Ala Asp Ile  
 290 295 300

Glu Gln Ile Tyr Lys Thr Cys Glu Pro Thr Lys Ala Leu Gly Gly His  
 305 310 315 320

Ala Gly Trp Ala Pro Phe Pro Val Arg Pro Arg Lys Arg His Thr Ser  
 325 330 335

Lys Thr Ser Tyr Met His Asp Glu Thr Met Asp Tyr Pro Phe Tyr Ala  
 340 345 350

Leu Thr Glu Thr Ile Asn Gly Ser Gly Pro Asn Gln Arg Gly Lys Tyr  
 355 360 365

Lys Ser Ala Tyr Met Ile Lys Asp Phe Pro Asp Phe Gln Ile Asp Val  
370 375 380

Ile Trp Lys Tyr Leu Thr Glu Val Pro Asp Gly Leu Thr Ser Ala Glu  
385 390 395 400

Met Lys Asp Ala Leu Leu Gln Val Asp Met Phe Gly Gly Glu Ile His  
405 410 415

Lys Val Val Trp Asp Ala Thr Ala Val Ala Gln Arg Glu Tyr Ile Ile  
420 425 430

Lys Leu Gln Tyr Gln Thr Tyr Trp Gln Glu Glu Asp Lys Asp Ala Val  
435 440 445

Asn Leu Lys Trp Ile Arg Asp Phe Tyr Glu Glu Met Tyr Glu Pro Tyr  
450 455 460

Gly Gly Val Pro Asp Pro Asn Thr Gln Val Glu Ser Gly Lys Gly Val  
465 470 475 480

Phe Glu Gly Cys Tyr Phe Asn Tyr Pro Asp Val Asp Leu Asn Asn Trp  
485 490 495

Lys Asn Gly Lys Tyr Gly Ala Leu Glu Leu Tyr Phe Leu Gly Asn Leu  
500 505 510

Asn Arg Leu Ile Lys Ala Lys Trp Leu Trp Asp Pro Asn Glu Ile Phe  
515 520 525

Thr Asn Lys Gln Ser Ile Pro Thr Lys Pro Leu Lys Glu Pro Lys Gln  
530 535 540

Thr Lys  
545

<210> 24

<211> 5

<212> PRT

<213> Schwanniomyces occidentalis

<400> 24

Ser Ala Ile Gln Ala

1 5

<210> 25

<211> 5

<212> PRT

<213> Artificial

<220>

<223> synthetic signal sequence

<400> 25

Met Ala Thr Leu Pro

1 5

<210> 26

<211> 4

<212> PRT

<213> Artificial

<220>

<223> synthetic signal sequence

<400> 26

Ala Thr Leu Pro

1

<210> 27

<211> 6

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 27

Lys Arg Glu Ala Glu Ala

1 5

<210> 28

<211> 5

<212> PRT

<213> *Aspergillus oryzae*

<400> 28

Ala Pro Ala Leu Ala

1 5